

REMARKS

Entry of this Amendment is proper because it narrows the issues on appeal and does not require further searching by the Examiner.

Claims 1-30 are all the claims presently pending in the application. Claims 1, 2, 10-12, 16, 19-20, 23-24, 26, 29 and 30 have been amended.

It is noted that the claim amendments herein or later are not made to distinguish the invention over the prior art or narrow the claims or for any statutory requirements of patentability. Further, Applicant specifically states that no amendment to any claim herein or later should be construed as a disclaimer of any interest in or right to an equivalent of any element or feature of the amended claim.

Applicant notes that claims 12 and 24 are not subject to any prior art rejection and therefore, would presumably be allowable if rewritten in independent form. However, Applicant respectfully submits that all of the claims are allowable.

Claims 1-30 stand rejected under 35 USC 112, first paragraph as allegedly failing to comply with the written description requirement. Applicant notes that the claims have been amended to address the Examiner's concerns and, therefore, these claims clearly comply with the written description requirement. In view of the foregoing, the Examiner is respectfully requested to withdraw this rejection.

Claims 1-8, 10, 11, 13-23, 25 and 27-29 stand rejected under 35 U.S.C. §103(a) as being allegedly unpatentable over Ganguly et al. (Proximal: A Database System for the Efficient Retrieval of Genetic Information", *Comput. Biol. Med.* Vol. 26, No 3, pp 199-207, 1996) (hereinafter "Ganguly") in view of Rigoutsos et al. ("Building Dictionaries of 1D and 3D Motifs by Mining The Unaligned 1D sequences of 17 Archaeal and Bacterial Genomes", 1999) (hereinafter "Rigoutsos '99"). **Claims 9, 26 and 30** stand rejected under 35 U.S.C. §103(a) as allegedly unpatentable over Ganguly and Rigoutsos '99, and further in view of Delcher et al. ("Improved Microbial Gene Identification with GLIMMER", 1999) (hereinafter "Delcher").

These rejections are respectfully traversed in the following discussion.

I. THE CLAIMED INVENTION

The claimed invention (e.g., as recited in claim 1) is directed to a system for identifying genes. The system includes a pattern database comprising patterns of amino acids, and an input device for inputting a genomic DNA sequence. The system further includes a processor which translates an open reading frame (ORF) of the DNA sequence into an amino acid translation, and locates in the amino acid translation occurrences of the patterns from the pattern database.

Importantly, the processor determines whether the open reading frame includes a putative gene based on a number of the patterns of amino acids located in the amino acid translation of the ORF, and/or weighted values associated with the patterns of amino acids located in the amino acid translation of the ORF (Application at page 13, lines 2-19).

Conventional systems for identifying genes (e.g., putative genes) are either based on the use the statistics of DNA sequences, or the use of similarity searches to determine gene locations (Application at page 2, lines 7-22). However, these conventional methods have various problems which prevent them from efficiently identifying genes in a given DNA sequence (Application at page 3, line 19-page 4, line 21).

The claimed invention, on the other hand, includes a processor which determines whether the open reading frame includes a putative gene **based on a number of the patterns of amino acids located in the amino acid translation of the ORF, and/or weighted values associated with the patterns** of amino acids located in the amino acid translation of the ORF (Application at page 13, lines 2-19). The claimed invention may be considered as including the best characteristics of statistical approaches and database similarity searches, in identifying genes in a given DNA sequence (Application at page 6, lines 18-21).

II. THE ALLEGED PRIOR ART REFERENCES

A. Ganguly and Rigoutsos '99

The Examiner alleges that Ganguly would have been combined with Rigoutsos '99 to form the invention of claims 1-8, 10, 11, 13-23, 25 and 27-29. Applicant submits, however, that Ganguly would not have been combined with Rigoutsos '99 and even if combined, the

combination would not teach or suggest each and every feature of the claimed invention.

Ganguly discloses a database system which allows complex sequence queries, interspersing similarity-type specifications with features such as constraints on the values of compositional parameters, defined features such as open reading frames and repeats and experimentally determined features such as DNA binding sites (Ganguly at page 200, lines 30-35).

Rigoutsos '99 shows that given large collections of amino acid sequences one can building dictionaries of amino acid sequence motifs from these collections and discusses a process for doing this. Attached hereto as Exhibit 1 is a flowchart illustrating the process of Rigoutsos '99.

Applicant respectfully submits that contrary to the Examiner's allegations, neither Ganguly, nor Rigoutsos '99, nor any alleged combination thereof, teaches or suggests a processor which "*determines whether said open reading frame includes a putative gene **based on a number of said patterns of amino acids located in said amino acid translation of said ORF, and/or weighted values associated with said patterns of amino acids located in said amino acid translation of said ORF***", as recited, for example, in claim 1, and similarly recited in claims 16, 23 and 29 (Application at page 13, lines 2-19).

Clearly, these features are not taught or suggested by the Ganguly or Rigoutsos '99. Indeed, the Examiner concedes on page 3 of the Office Action that Ganguly does not teach or suggest this feature. The Examiner alleges that Rigoutsos '99 discloses this feature, but the Examiner is incorrect.

In fact, as Applicant has repeatedly pointed out to the Examiner, Rigoutsos '99 discloses a method of creating a pattern database. Rigoutsos '99 does not teach or suggest using the pattern database, and certainly does not teach or suggest using the pattern database to identify genes.

On page 10 of the Office Action, the Examiner attempts to rely on pages 224, 226 and 228 in Rigoutsos '99 to support his position. However, this is completely unreasonable.

Indeed, on page 224, Rigoutsos '99 simply discloses a database containing ORFs for complete genomes and a method of using a pattern discovery algorithm (e.g., Teiresias) to form a

pattern database, and on page 226, Rigoutsos '99 simply discloses the experimental results from using Teiresias algorithm to discover patterns.

Further, Applicant would again point out that page 228, col. 2, lines 4-11 in Rigoutsos '99 merely reads (in pertinent part)

"[o]ne of the seqlets that are discovered when we process the input database is and is present in the following ten ORFs: Of these, gi_3328856 and gi_3329230 are annotated as Fe-S oxidoreductases."

That is, this short and simple passage does not teach or suggest determining whether the open reading frame includes a putative gene **based on a number of the patterns of amino acids located in the amino acid translation of the ORF, and/or weighted values associated with the patterns** of amino acids located in the amino acid translation of the ORF

Indeed, Applicant would again point out that the passage at page 228, col. 2, lines 4-11 in Rigoutsos '99 clearly does not teach or suggest locating occurrences of patterns from the pattern database in the amino acid translation. In fact, nowhere does this passage discuss "locating" anything, let alone locating occurrences of "patterns" in an amino acid translation of some DNA sequence. Indeed, in its entirety, the discussion of Rigoutsos '99 revolves around amino acid sequences: all of the discussed datasets comprise amino acid sequences.

That is, **nowhere does Rigoutsos '99 even mention DNA sequences.** Therefore, it is completely unreasonable for the Examiner to allege that Rigoutsos '99 teaches determining whether the open reading frame includes a putative gene **based on a number of the patterns of amino acids located in the amino acid translation of the ORF, and/or weighted values associated with the patterns** of amino acids located in the amino acid translation of the ORF.

Therefore, Applicant submits that these alleged references would not have been combined and even if combined, the combination would not teach or suggest each and every element of the claimed invention. Therefore, the Examiner is respectfully requested to withdraw this rejection.

B. Delcher

The Examiner alleges that Ganguly and Rigoutsos would have been further combined

with Delcher to form the invention of claims 9, 26 and 30. Applicant submits, however, that these alleged references would not have been combined and even if combined, the combination would not teach or suggest each and every feature of the claimed invention.

Applicant respectfully submits that these references would not have been combined as alleged by the Examiner. Indeed, these references are unrelated, and no person of ordinary skill in the art would have considered combining these disparate references, absent impermissible hindsight.

In fact, these references clearly do not teach or suggest their combination. Therefore, Applicant respectfully submits that one of ordinary skill in the art would not have been so motivated to combine the references as alleged by the Examiner. Therefore, the Examiner has failed to make a prima facie case of obviousness.

Moreover, contrary to the Examiner's allegations, neither Ganguly, nor Rigoutsos nor Delcher, nor any combination thereof teaches or suggests a processor that "*determines whether said open reading frame includes a putative gene based on a number of said patterns of amino acids located in said amino acid translation of said ORF, and/or weighted values associated with said patterns of amino acids located in said amino acid translation of said ORF*", as recited, for example, in claim 1, and similarly recited in claims 16, 23 and 29 (Application at page 13, lines 2-19).

Clearly, Delcher does not teach or suggest these features of the claimed invention. Indeed, the Examiner attempts to rely on pages 4639 and 4640 in Delcher to support his position. However, this is clearly unreasonable. Indeed, these passages in Delcher simply disclose doing a comparison in the space of nucleotide sequences, and if its nucleotide sequences matches the expectation in terms of nucleotide sequence composition as the latter is captured by the HMM, then an ORF is reported as a putative gene.

That is, nowhere does Delcher teach or suggest determining whether the open reading frame includes a putative gene **based on a number of the patterns of amino acids located in the amino acid translation of the ORF, and/or weighted values associated with the patterns**

of amino acids located in the amino acid translation of the ORF.

Therefore, Delcher does not make up for the deficiencies in Ganguly and Rigoutsos '99.

Therefore, Applicant submits that these alleged references would not have been combined and even if combined, the combination would not teach or suggest each and every element of the claimed invention. Therefore, the Examiner is respectfully requested to withdraw this rejection.

IV. FORMAL MATTERS AND CONCLUSION

In view of the foregoing, Applicant submits that claims 1-30, all the claims presently pending in the application, are patentably distinct over the prior art of record and are in condition for allowance. The Examiner is respectfully requested to pass the above application to issue at the earliest possible time.

Should the Examiner find the application to be other than in condition for allowance, the Examiner is requested to contact the undersigned at the local telephone number listed below to discuss any other changes deemed necessary in a telephonic or personal interview.

The Commissioner is hereby authorized to charge any deficiency in fees or to credit any overpayment in fees to Assignee's Deposit Account No. 50-0510.

Respectfully Submitted,

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